

(19) World Intellectual Property Organization
International Bureau



(43) International Publication Date
4 October 2001 (04.10.2001)

PCT

(10) International Publication Number
WO 01/073134 A3

- (51) International Patent Classification⁷: **C12Q 1/68**
- (21) International Application Number: **PCT/US01/09993**
- (22) International Filing Date: **28 March 2001 (28.03.2001)**
- (25) Filing Language: **English**
- (26) Publication Language: **English**
- (30) Priority Data:
60/192,700 **28 March 2000 (28.03.2000)** **US**
- (71) Applicant (*for all designated States except US*): **THE GOVERNMENT OF THE UNITED STATES OF AMERICA**, as represented by **THE SECRETARY, DEPARTMENT OF HEALTH & HUMAN SERVICES, THE NATIONAL INSTITUTES OF HEALTH [US/US]**; Office Of Technology Transfer, 6011 Executive Boulevard, Suite #325, Rockville, MD 20852 (US).
- (72) Inventors; and
- (75) Inventors/Applicants (*for US only*): **WANG, Ena** [CN/US]; 4500 Gretna Street, Bethesda, MD 20814 (US). **MARINCOLA, Francesco, M.** [US/US]; 10110 Chapel Road, Potomac, MD 20854 (US). **MILLER, Lance, D.** [US/US]; 13109-E Millhaven Place, Germantown, MD 20874 (US).
- (81) Designated States (*national*): **AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW.**
- (84) Designated States (*regional*): **ARIPO** patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), **Eurasian** patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), **European** patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), **OAPI** patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).
- Published:**
— *with international search report*
- (88) Date of publication of the international search report:
16 January 2003
- For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.*

(54) Title: **GENE PROFILING ARRAYS**

(57) Abstract: Ordered arrays of mixtures of nucleic acid molecules are provided, which mixtures reflect the expression profile of one or more specimens, such as different cells or tissues. In particular embodiments, complete mRNA mixtures from specimens are separately arrayed on a substrate. Specimens from which such mixtures of nucleic acid molecules are produced can be taken from any source, including animal, plant and/or microbial cells, and can be assembled in any collection desired. The collections can, for instance, include different cell types, different phenotypes, cells grown under different conditions, cells of different ages or developmental stages, and so forth. The nucleic acid arrays are provided in both macro- and microarray formats, and are suitable for gene profiling in which relative quantitative expression from a single source or multiple sources may be determined. Techniques are also disclosed for producing high-fidelity, amplified mixtures of nucleic acid molecules using a combination of anti-sense RNA amplification and template-switching synthesis. Amplified mixtures produced using this method can, for instance, be applied to the disclosed arrays. The disclosed arrays allow high throughput analysis of differential gene expression in a specimen (such as a tumor) or a variety of specimens (such as a variety of tumors), and are suitable for automated preparation and analysis.

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